SEQUENCE LISTING

<110> Her Majesty the Queen in Right of Canada as Represented by the Minister of Agriculture and Agri-Food

<120> Regulation Of Gene Expression Using Chromatin Remodelling Factors

<130> 08-890985WO

<150> US 60/387,088

<151> 2002-06-06

<160> 104

<170> PatentIn version 3.0

<210> 1

<211> 142

<212> PRT

<213> WT-ROS

<400> 1

Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu
1   5   10   15

Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
                20   25   30

Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly
            35   40   45

Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro
        50   55   60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu
65   70   75   80

Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
                85   90   95

His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Val

```
                    100                    105                    110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
        115                    120                    125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg
    130                    135                    140
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<210> 2

<211> 472

<212> DNA

<213> synthetic ROS

<400> 2

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gcggatcccc gggtatgact gagactgctt acggtaacgc tcaggatctt cttgttgagc     60

ttactgctga tatcgttgct gcttacgttt ctaaccacgt tgttcctgtt actgagcttc    120

ctggacttat ctctgatgtt catactgcac tttctggaac atctgctcct gcttctgttg    180

ctgttaacgt tgagaagcag aagcctgctg tttctgttcg taagtctgtt caggatgatc    240

atatcgtttg tttggagtgt ggtggttctt tcaagtctct caagcgtcac cttactactc    300

atcactctat gactccagag gagtatagag agaagtggga tcttcctgtt gattacccta    360

tggttgctcc tgcttacgct gaggctcgtt ctcgtctcgc taaggagatg ggtctcggtc    420

agcgtcgtaa ggctaaccgt ccaaaaaaga agcgtaaggt ctgagagctc gc            472
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<210> 3

<211> 447

<212> DNA

<213> concensus

<220>

<221> misc_feature

<222> (1)..(447)

<223> where n is "a" or "c" or "t" or "g"

<220>

<221> misc_feature

<222> (1)..(447)

<223> where d is "a" or "t" or "g"

<220>

<221> misc_feature

<222> (1)..(447)

<223> where v is "a" or "c" or "g"

<220>

<221> misc_feature

<222> (1)..(447)

<223> where k is "t" or "g"

<220>

<221> misc_feature

<222> (1)..(447)

<223> where s is "c" or "g"

<220>

<221> misc_feature

<222> (1)..(447)

<223> where w is "a" or "t"

<220>

<221> misc_feature

<222> (1)..(447)

<223> where h is "a" or "t" or "c"

<220>

<221> misc_feature

<222> (1)..(447)

<223> where b is "t" or "c" or "g"

<220>

<221>   misc_feature

<222>   (1)..(447)

<223>   where r is "a" or "g"

<220>

<221>   misc_feature

<222>   (1)..(447)

<223>   where y is "c" or "t"

<220>

<221>   misc_feature

<222>   (1)..(447)

<223>   where m is "a" or "c"

<400>   3
atgacncgara cngcntaygg naaygcncar gayytnytng tngarytnac ngcngayath   60

gtngcngcnt aygtnwsnaa ycaygtngtn ccngtnacng arytnccngg nytnathwsn   120

gaygtncaya cngcnytnws nggnacnwsn gcnccngcnw sngtngcngt naaygtngar   180

aarcaraarc cngcngtnws ngtnmgnaar wsngtncarg aygaycayat hgtntgyytn   240

gartgyggng gnwsnttyaa rwsnytnaar mgncayytna cnacncayca ywsnatgacn   300

ccngargart aymgngaraa rtgggayytn ccngtngayt ayccnatggt ngcnccngcn   360

taygcngarg cnmgnwsnmg nytngcnaar garatgggny tnggncarmg nmgnaargcn   420

aaymgnccna araaraarmg naargtn   447

<210>   4

<211>   149

<212>   PRT

<213>   synthetic ROS

<400>   4

Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu

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  1                 5                    10                   15

Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
             20                  25              30

Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly
         35              40              45

Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro
     50              55                  60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu
65               70                  75                       80

Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
             85              90                       95

His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Val
             100             105             110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
         115             120             125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg Pro Lys
     130             135             140

Lys Lys Arg Lys Val
145
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<210> 5

<211> 10

<212> PRT

<213> ROS binding

<400> 5

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Trp Ala Thr Asp His Trp Lys Met Ala Arg
1               5               10
```

<210> 6

<211> 7

<212> PRT

<213> NLS

<400> 6

```
Pro Lys Lys Lys Arg Lys Val
1               5
```

<210> 7

<211> 25

<212>   DNA

<213>   ROS operator

<400>   7   25
tatatttcaa ttttattgta atata

<210>   8

<211>   27

<212>   DNA

<213>   IPT gene operator

<400>   8   27
tataattaaa atattaactg tcgcatt

<210>   9

<211>   11

<212>   DNA

<213>   operator sequence binding to ERF

<400>   9   11
taagagccgc c

<210>   10

<211>   9

<212>   DNA

<213>   operator sequence binding to SEBF

<400>   10   9
gactgtcac

<210>   11

<211>   9

<212>   DNA

<213>   operator sequence binding to CBF

<400> 11
taccgacat   9

<210> 12

<211> 8

<212> DNA

<213> operator sequence binding to CBF

<400> 12
tggccgac   8

<210> 13

<211> 16

<212> PRT

<213> NLS of AGAMOUS protein

<400> 13

Arg Ile Glu Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg
1   5   10   15

<210> 14

<211> 18

<212> PRT

<213> NLS of TGA-1A protein

<400> 14

Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg
1   5   10   15

Lys Lys

<210> 15

<211> 21

<212> PRT

<213> NLS of TGA-1B protein

<400> 15

```
Lys Lys Arg Ala Arg Leu Val Arg Asn Arg Glu Ser Ala Gln Leu Ser
1               5                   10                  15

Arg Gln Arg Lys Lys
            20
```

<210> 16

<211> 18

<212> PRT

<213> NLS of O2 NLS B protein

<400> 16

```
Arg Lys Arg Lys Glu Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Tyr
1               5                   10                  15

Arg Lys
```

<210> 17

<211> 45

<212> PRT

<213> NLS of NIa protein

<220>

<221> LIPID

<222> (1)..(45)

<223> where "x" is any amino acid

<400> 17

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Lys Lys Asn Gln Lys His Lys Leu Lys Met Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Arg Lys
        35                  40              45
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<210> 18

<211> 16

<212> PRT

<213> NLS nucleoplasmin protein

<400> 18

Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
1   5   10   15

<210> 19

<211> 17

<212> PRT

<213> NLS of NO38 protein

<400> 19

Lys Arg Ile Ala Pro Asp Ser Ala Ser Lys Val Pro Arg Lys Lys Thr
1   5   10   15

Arg

<210> 20

<211> 17

<212> PRT

<213> NLS of N1/N2 protein

<400> 20

Lys Arg Lys Thr Glu Glu Glu Ser Pro Leu Lys Asp Lys Asp Ala Lys
1   5   10   15

Lys

<210> 21

<211> 17

<212> PRT

<213> NLS of Glucocorticoid receptor

<400> 21

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys
1   5   10   15

Lys

<210> 22

<211> 17

<212> PRT

<213> NLS of Glucocorticoid a receptor

<400> 22

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys
1   5   10   15

Lys

<210> 23

<211> 17

<212> PRT

<213> NLS of Glucocorticoid b receptor

<400> 23

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys
1   5   10   15

Lys

<210> 24

<211> 17

<212> PRT

<213> NLS of Progesterone receptor

<400> 24

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
1   5   10   15

Lys

<210> 25

<211> 17

<212> PRT

<213> NLS of Androgen receptor

<400> 25

Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys
1   5   10   15

Lys

<210> 26

<211> 17

<212> PRT

<213> NLS of p53 protein

<400> 26

Arg Arg Cys Phe Glu Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg
1   5   10   15

Lys

<210> 27

<211> 25

<212> DNA

<213> VirC/VirD operator sequence

<400> 27
tatatttcaa ttttattgta atata   25

<210> 28

<211> 108

<212> DNA

<213> ROS-OPDS

<400> 28
atctccactg acgtaaggga tgacgcacaa tcccactatc cttcgcaaga cccttcctct   60

atataatata tttcaatttt attgtaatat aacacggggg actctaga   108

<210> 29

<211> 113

<212> DNA

11

<213>   ROS-OPDA

<400>   29
gatcctctag agtcccccgt gttatattac aataaaattg aaatatatta tatagaggaa   60

gggtcttgcg aaggatagtg ggattgtgcg tcatccctta cgtcagtgga gat   113

<210>   30

<211>   107

<212>   DNA

<213>   ROS-OPUS

<400>   30
atctccactg acgtaaggga tgacgcacaa tctatatttc aattttattg taatatacta   60

tataaggaag ttcatttcat ttggagagaa cacgggggac tctagag   107

<210>   31

<211>   111

<212>   DNA

<213>   ROS-OPUA

<400>   31
gatcctctag agtcccccgt gttctctcca aatgaaatga acttccttat atagtatatt   60

acaataaaat tgaaatatag attgtgcgtc atcccttacg tcagtggaga t   111

<210>   32

<211>   108

<212>   DNA

<213>   ROS-OPPS

<400>   32
atctccactg acgtaaggga tgacgcacaa tctatatttc aattttattg taatatacta   60

tataatatat ttcaatttta ttgtaatata acacggggga ctctagag   108

<210>   33

<211>   112

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<212>   DNA

<213>   ROS-OPPA


<400>   33
gatcctctag agtcccccgt gttatattac aataaaattg aaatatatta tatagtatat        60

tacaataaaa ttgaaatata gattgtgcgt catcccttac gtcagtggag at              112


<210>   34

<211>   59

<212>   DNA

<213>   ROS-OP1


<400>   34
gatcctatat ttcaatttta ttgtaatata gctatatttc aattttattg taatataat        59


<210>   35

<211>   57

<212>   DNA

<213>   ROS-OP2


<400>   35
cgattatatt acaataaaat tgaaatatag ctatattaca ataaaattga aatatag          57


<210>   36

<211>   36

<212>   DNA

<213>   tms2 promoter sense primer


<400>   36
tgcggatgca taagcttgct gacattgcta gaaaag                                 36


<210>   37

<211>   26

<212>   DNA

<213>   tms2 promoter anti-sense primer
```

13

<400> 37
cggggatcct ttcagggcca tttcag   26

<210> 38

<211> 24

<212> DNA

<213> actin2 promoter sense primer

<400> 38
aagcttatgt atgcaagagt cagc   24

<210> 39

<211> 24

<212> DNA

<213> actin2 promoter anti-sense primer

<400> 39
ttgactagta tcagcctcag ccat   24

<210> 40

<211> 138

<212> DNA

<213> EcoRV to ATG of GUS

<400> 40
gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca agacccttcc   60

tctatataat atatttcaat tttattgtaa tataacacgg gggactctag aggatccccg   120

ggtggtcagt cccttatg   138

<210> 41

<211> 136

<212> DNA

<213> EcoRV to ATG of GUS

<400> 41

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gatatctcca ctgacgtaag ggatgacgca caatctatat ttcaatttta ttgtaatata      60

ctatataagg aagttcattt catttggaga gaacacgggg gactctagag gatccccggg     120

tggtcagtcc cttatg                                                     136
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<210> 42

<211> 137

<212> DNA

<213> EcoRV to ATG of GUS


```
<400> 42
gatatctcca ctgacgtaag ggatgacgca caatctatat ttcaatttta ttgtaatata      60

ctatataata tatttcaatt ttattgtaat ataacacggg ggactctaga ggatccccgg     120

gtggtcagtc ccttatg                                                    137
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<210> 43

<211> 237

<212> DNA

<213> EcoRV to ATG of GUS


```
<400> 43
gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca agacccttcc      60

tctatataat atatttcaat tttattgtaa tataacacgg gggactctag aggatcctat     120

atttcaattt tattgtaata tagctatatt tcaattttat tgtaatataa tcgatttcga     180

acccggggta ccgaattcct cgagtctaga ggatccccgg gtggtcagtc ccttatg        237
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<210> 44

<211> 31

<212> DNA

<213> forward primer for HDA19 A. thaliana, pDBLeu-HDA19


```
<400> 44
gcgtcgacga tggatactgg cggcaattcg c                                     31
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<210> 45

<211> 32

<212>   DNA

<213>   reverse primer for HDA19 A. thaliana, pDBLeu-HDA19

<400>   45
aggcggccgc ttatgtttta ggaggaaacg cc   32

<210>   46

<211>   31

<212>   DNA

<213>   forward primer for Gen5 Arabidopsis, GST-Gen5

<400>   46
gcgtcgacga tggactctca ctcttcccac c   31

<210>   47

<211>   31

<212>   DNA

<213>   reverse primer for Gen5 Arabidopsis, GST-Gen5

<400>   47
gcgcggccgc ctattgagat ttagcaccag a   31

<210>   48

<211>   31

<212>   DNA

<213>   reverse primer forHDA19, GST-HDA19

<400>   48
gcgcggccgc ttatgtttta ggaggaaacg c   31

<210>   49

<211>   29

<212>   DNA

<213>   forward primer for bnKCP1, 1-80, 1-160 (generation of mutants)

```
<400>  49
gcaagcttat ggcaggagga ggaccaact                                    29


<210>  50

<211>  29

<212>  DNA

<213>  reverse primer for bnKCP1 1-160 (generation of mutants)


<400>  50
cgctcgagct cctcctcatc attgtcttc                                    29


<210>  51

<211>  29

<212>  DNA

<213>  reverse primer for bnKCP1 1-80 (generation of mutants)


<400>  51
cgctcgagat gaacaggcaa aagaggcat                                    29


<210>  52

<211>  29

<212>  DNA

<213>  reverse primer for bnKCP1 (generation of mutants)
  \

<400>  52
cgctcgagct catcttcttc ttcttcttc                                    29


<210>  53

<211>  30

<212>  DNA

<213>  forward primer for bnKCP1, 1-80 and 1-160 (in vivo assay and
transactivation assay)


<400>  53
gcgtcgacga tggcaggagg aggaccaact                                   30


<210>  54
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<211> 31

<212> DNA

<213> reverse primer for bnKCP1

<400> 54
gcgcggccgc ctcatcttct tcttcttcct c   31

<210> 55

<211> 31

<212> DNA

<213> reverse primer for bnKCP1

<400> 55
gcgcggccgc atgaacaggc aaaagaggca t   31

<210> 56

<211> 31

<212> DNA

<213> reverse primer for bnKCP1

<400> 56
gcgcggccgc ctcctcctca tcattgtctt c   31

<210> 57
<211> 45

<212> DNA

<213> forward primer for bnKCP1G188

<400> 57
gatgttcttg cgaggagacc aggattcaag aacagagcat tgaag   45

<210> 58

<211> 45

<212> DNA

<213> reverse primer for bnKCP1G188

<400> 58
cttcaatgct ctgttcttga atcctggtct cctcgcaaga acatc   45

<210> 59

<211> 30

<212> DNA

<213> forward primer for bnKCP1 81-215

<400> 59
gcgtcgacgc tagggttggc ttcattgaga   30

<210> 60

<211> 29

<212> DNA

<213> forward primer for entire encoding region of bnKCP1

<400> 60
gcgaattcat ggcaggagga ggaccaact   29

<210> 61

<211> 29

<212> DNA

<213> reverse primer for entire coding region of bnKCP1

<400> 61
cggagctcct catcttcttc ttcttcttc   29

<210> 62

<211> 7

<212> PRT

<213> pat7 NLS (PLNKKRR)

<400> 62

Pro Leu Asn Lys Lys Arg Arg
1   5

<210> 63

19

<211> 143

<212> PRT

<213> aa seq of ROSR (ROS receptor)

<400> 63

```
Met Thr Asp Met Ala Thr Gly Asn Ala Pro Glu Leu Leu Val Glu Leu
1               5                   10                  15

Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
            20                  25                  30

Ser Asp Leu Ala Asn Leu Ile Ser Asp Val His Ser Ala Leu Ser Asn
        35                  40                  45

Thr Ser Val Pro Gln Pro Ala Ala Val Val Glu Lys Gln Lys Pro
    50                  55                  60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Glu Gln Ile Thr Cys Leu
65                  70                  75                  80

Glu Cys Gly Gly Asn Phe Lys Ser Leu Lys Arg His Leu Met Thr His
                85                  90                  95

His Ser Leu Ser Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Thr
            100                 105                 110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
    115                 120                 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Arg Gly Arg Gly
    130                 135                 140
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<210> 64

<211> 142

<212> PRT

<213> aa seq of ROSAR (ROS receptor)

<400> 64

```
Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu
1               5                   10                  15

Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
            20                  25                  30

Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly
        35                  40                  45

Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro
    50                  55                  60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu
```

```
     65                    70                    75                    80

Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
                85                    90                    95

His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Gln Val
               100                   105                   110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
           115                   120                   125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg
   130                   135                   140
```

<210>   65

<211>   143

<212>   PRT

<213>   aa seq of MucR (ROS receptor)

<400>   65

```
Met Thr Glu Thr Ser Leu Gly Thr Ser Asn Glu Leu Leu Val Glu Leu
1               5                    10                    15

Thr Ala Glu Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
                20                    25                    30

Ala Glu Leu Pro Thr Leu Ile Ala Asp Val His Ser Ala Leu Asn Asn
               35                    40                    45

Thr Thr Ala Pro Ala Pro Val Val Val Pro Val Glu Lys Pro Lys Pro
   50                    55                    60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp Gln Ile Thr Cys Leu
65                    70                    75                    80

Glu Cys Gly Gly Thr Phe Lys Ser Leu Lys Arg His Leu Met Thr His
                85                    90                    95

His Asn Leu Ser Pro Glu Glu Tyr Arg Asp Lys Trp Asp Leu Pro Ala
               100                   105                   110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
           115                   120                   125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Arg Arg Gly Lys
   130                   135                   140
```

<210>   66

<211>   10

<212>   DNA

<213>   VirC/VirD DNA binding site seq (1)

21

<400> 66
tatatttcaa   10

<210> 67

<211> 10

<212> DNA

<213> VirC/VirD DNA binding site seq (2)

<400> 67
tatattacaa   10

<210> 68

<211> 10

<212> DNA

<213> ipt DNA binding site seq (1)

<400> 68
tataattaaa   10

<210> 69

<211> 10

<212> DNA

<213> ipt DNA binding site seq (2)

<400> 69
aatgcgacag   10

<210> 70

<211> 10

<212> DNA

<213> concensus DNA binding site seq

<400> 70
tatahttcaa   10

<210> 71

<211> 215

<212> PRT

<213> bnKCP aa seq

<400> 71

Met Ala Gly Gly Gly Pro Thr Phe Ser Ile Glu Leu Ser Ala Tyr Gly
1   5   10   15

Ser Asp Leu Pro Thr Asp Lys Ala Ser Gly Asp Ile Pro Asn Glu Glu
            20   25   30

Gly Ser Gly Leu Ser Arg Val Gly Ser Gly Ile Trp Ser Gly Arg Thr
        35   40   45

Val Asp Tyr Ser Ser Glu Ser Ser Ser Ile Gly Thr Pro Gly Asp
    50   55   60

Ser Glu Glu Glu Asp Glu Glu Ser Glu Glu Asp Asn Asp Glu Glu Glu
65   70   75   80

Leu Gly Leu Ala Ser Leu Arg Ser Leu Glu Asp Ser Leu Pro Ser Lys
                85   90   95

Gly Leu Ser Ser His Tyr Lys Gly Lys Ser Lys Ser Phe Gly Asn Leu
            100   105   110

Gly Glu Ile Gly Ser Val Lys Glu Val Pro Lys Gln Glu Asn Pro Leu
            115   120   125

Asn Lys Lys Arg Arg Leu Gln Ile Tyr Asn Lys Leu Ala Arg Lys Ser
            130   135   140

Phe Tyr Ser Trp Gln Asn Pro Lys Ser Met Pro Leu Leu Pro Val His
145   150   155   160

Glu Asp Asn Asp Asp Glu Glu Gly Asp Asp Gly Asp Leu Ser Asp Glu
                165   170   175

Glu Arg Gly Gly Asp Val Leu Ala Arg Arg Pro Ser Phe Lys Asn Arg
            180   185   190

Ala Leu Lys Ser Met Ser Cys Phe Ala Leu Ser Asp Leu Gln Glu Glu
            195   200   205

Glu Glu Glu Glu Glu Asp Glu
    210   215

<210> 72

<211> 240

<212> PRT

<213> atKCP aa seq

23

<400> 72

Met	Glu	Leu	Met	Ala	Lys	Pro	Thr	Phe	Ser	Ile	Glu	Val	Ser	Gln	Tyr

Met Glu Leu Met Ala Lys Pro Thr Phe Ser Ile Glu Val Ser Gln Tyr
1   5   10   15

Gly Thr Thr Asp Leu Pro Ala Thr Glu Lys Ala Ser Ser Ser Ser Ser
            20   25   30

Ser Phe Glu Thr Thr Asn Glu Glu Gly Val Glu Glu Ser Gly Leu Ser
        35   40   45

Arg Ile Trp Ser Gly Gln Thr Ala Asp Tyr Ser Ser Asp Ser Ser Ser
    50   55   60

Ile Gly Thr Pro Gly Asp Ser Glu Glu Asp Glu Glu Glu Ser Glu Asn
65   70   75   80

Glu Asn Asp Asp Val Ser Ser Lys Glu Leu Gly Leu Arg Gly Leu Ala
                85   90   95

Ser Met Ser Ser Leu Glu Asp Ser Leu Pro Ser Lys Arg Gly Leu Ser
            100   105   110

Asn His Tyr Lys Gly Lys Ser Lys Ser Phe Gly Asn Leu Gly Glu Ile
        115   120   125

Gly Ser Val Lys Glu Val Ala Lys Gln Glu Asn Pro Leu Asn Lys Arg
    130   135   140

Arg Arg Leu Gln Ile Cys Asn Lys Leu Ala Arg Lys Ser Phe Tyr Ser
145   150   155   160

Trp Gln Asn Pro Lys Ser Met Pro Leu Leu Pro Val Asn Glu Asp Glu
                165   170   175

Asp Asp Asp Asp Glu Asp Asp Asp Glu Glu Asp Leu Lys Ser Gly Phe
                180   185   190

Asp Glu Asn Lys Ser Ser Ser Asp Glu Glu Gly Val Lys Lys Val Val
            195   200   205

Val Arg Lys Gly Ser Phe Lys Asn Arg Ala Tyr Lys Ser Arg Ser Cys
    210   215   220

Phe Ala Leu Ser Asp Leu Ile Glu Glu Glu Asp Asp Asp Asp Asp Gln
225   230   235   240

<210> 73

<211> 214

<212> PRT

<213> atKCL1 aa seq -

<400> 73

Met Glu Val Leu Val Gly Ser Thr Phe Arg Asp Arg Ser Ser Val Thr
1   5   10   15

Thr His Asp Gln Ala Val Pro Ala Ser Leu Ser Ser Arg Ile Gly Leu
            20   25   30

Arg Arg Cys Gly Arg Ser Pro Pro Pro Glu Ser Ser Ser Ser Val Gly
        35   40   45

Glu Thr Ser Glu Asn Glu Glu Asp Glu Asp Asp Ala Val Ser Ser Ser
    50   55   60

Gln Gly Arg Trp Leu Asn Ser Phe Ser Ser Ser Leu Glu Asp Ser Leu
65   70   75   80

Pro Ile Lys Arg Gly Leu Ser Asn His Tyr Ile Gly Lys Ser Lys Ser
            85   90   95

Phe Gly Asn Leu Met Glu Ala Ser Asn Thr Asn Asp Leu Val Lys Val
            100   105   110

Glu Ser Pro Leu Asn Lys Arg Arg Arg Leu Leu Ile Ala Asn Lys Leu
        115   120   125

Arg Arg Arg Ser Ser Leu Ser Ser Phe Ser Ile Tyr Thr Lys Ile Asn
    130   135   140

Pro Asn Ser Met Pro Leu Leu Ala Leu Gln Glu Ser Asp Asn Glu Asp
145   150   155   160

His Lys Leu Asn Asp Asp Asp Asp Asp Asp Ser Ser Ser Asp Asp
            165   170   175

Glu Thr Ser Lys Leu Lys Glu Lys Arg Met Lys Met Thr Asn His Arg
            180   185   190

Asp Phe Met Val Pro Gln Thr Lys Ser Cys Phe Ser Leu Thr Ser Phe
        195   200   205

Gln Asp Asp Asp Asp Arg
    210

<210> 74

<211> 221

<212> PRT

<213> atKCL2 aa seq

<400> 74

Met Val Gly Ser Ser Phe Gly Ile Gly Met Ala Ala Tyr Val Arg Asp
1   5   10   15

His Arg Gly Val Ser Ala Gln Asp Lys Ala Val Gln Thr Ala Leu Phe
            20   25   30

Leu Ala Asp Glu Ser Gly Arg Gly Gly Ser Gln Ile Gly Ile Gly Leu
        35   40   45

Arg Met Ser Asn Asn Asn Asn Lys Ser Pro Glu Glu Ser Ser Asp Ser
    50   55   60

25

Ser Ser Ser Ile Gly Glu Ser Ser Glu Asn Glu Glu Glu Glu Glu
65   70   75   80

Asp Asp Ala Val Ser Cys Gln Arg Gly Thr Leu Asp Ser Phe Ser Ser
             85   90   95

Ser Leu Glu Asp Ser Leu Pro Ile Lys Arg Gly Leu Ser Asn His Tyr
        100   105   110

Val Gly Lys Ser Lys Ser Phe Gly Asn Leu Met Glu Ala Ala Ser Lys
        115   120   125

Ala Lys Asp Leu Glu Lys Val Glu Asn Pro Phe Asn Lys Arg Arg Arg
     130   135   140

Leu Val Ile Ala Asn Lys Leu Arg Arg Arg Gly Arg Ser Ile Thr Tyr
145   150   155   160

Glu Glu Asp His His Ile His Asn Asp Asp Tyr Glu Asp Asp Asp Gly
             165   170   175

Asp Gly Asp Asp His Arg Lys Ile Met Met Met Met Lys Asn Lys Lys
        180   185   190

Glu Leu Met Ala Gln Thr Arg Ser Cys Phe Cys Leu Ser Ser Leu Gln
        195   200   205

Glu Glu Asp Asp Gly Asp Gly Asp Asp Asp Glu Asp Glu
     210   215   220

<210> 75

<211> 42

<212> PRT

<213> bnKCP aa seq

<400> 75

Gly Asp Asp Gly Asp Leu Ser Asp Glu Glu Arg Gly Gly Asp Val Leu
1   5   10   15

Ala Arg Arg Pro Ser Phe Lys Asn Arg Ala Leu Lys Ser Met Ser Cys
        20   25   30

Phe Ala Leu Ser Asp Leu Gln Glu Glu Glu
        35   40

<210> 76

<211> 42

<212> PRT

<213> ATF-1 aa seq

<400> 76

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Asp Ser Ser Asp Ser Ile Gly Ser Ser Gln Gln Ala His Gly Ile Leu
1               5                   10                  15

Ala Arg Arg Pro Ser Tyr Arg Lys Ile Leu Lys Asp Leu Ser Ser Glu
            20                  25                  30

Asp Thr Arg Gly Arg Lys Gly Asp Gly Glu
        35                  40
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<210> 77

<211> 42

<212> PRT

<213> hyCREB aa seq

<400> 77

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Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu
1               5                   10                  15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp
            20                  25                  30

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu
        35                  40
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<210> 78

<211> 42

<212> PRT

<213> CREB aa seq

<400> 78

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Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu
1               5                   10                  15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp
            20                  25                  30

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu
        35                  40
```

<210> 79

<211> 42

<212> PRT

<213> CREM aa seq

<400> 79

27

Ser Ala Asp Ser Glu Val Ile Asp Ser His Lys Arg Arg Glu Ile Leu
1   5   10   15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Glu Leu Ser Ser Asp
            20   25   30

Val Pro Gly Ile Pro Lys Ile Glu Glu Glu
        35   40

<210> 80

<211> 42

<212> PRT

<213> cCREM aa seq

<400> 80

Ala Glu Ser Glu Gly Val Ile Asp Ser His Lys Arg Arg Glu Ile Leu
1   5   10   15

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Glu Leu Ser Ser Asp
            20   25   30

Val Pro Gly Val Pro Lys Ile Glu Glu Glu
        35   40

<210> 81

<211> 461

<212> PRT

<213> aa seq of BNSCL1

<400> 81

Met Lys Leu Gln Ala Ser Ser Pro Gln Asp Asn Gln Pro Ser Asn Thr
1   5   10   15

Thr Asn Asn Ser Thr Asp Ser Asn His Leu Ser Met Asp Glu His Ala
            20   25   30

Met Arg Ser Met Asp Trp Asp Ser Ile Met Lys Glu Leu Glu Val Asp
        35   40   45

Asp Asp Ser Ala Pro Tyr Gln Leu Gln Pro Ser Ser Phe Asn Leu Pro
    50   55   60

Val Phe Pro Asp Ile Asp Ser Ser Asp Val Tyr Pro Gly Pro Asn Gln
65   70   75   80

Ile Thr Gly Tyr Gly Phe Asn Ser Leu Asp Ser Val Asp Asn Gly Gly
            85   90   95

Phe Asp Tyr Ile Glu Asp Leu Ile Arg Val Val Asp Cys Ile Glu Ser
            100   105   110

```
Asp Glu Leu His Leu Ala His Val Val Leu Ser Gln Leu Asn Gln Arg
        115                 120                 125

Leu Gln Thr Ser Ala Gly Arg Pro Leu Gln Arg Ala Ala Phe Tyr Phe
        130                 135                 140

Lys Glu Ala Leu Gly Ser Leu Leu Thr Gly Thr Asn Arg Asn Gln Leu
145                 150                 155                 160

Phe Ser Trp Ser Asp Ile Val Gln Lys Ile Arg Ala Ile Lys Glu Phe
                165                 170                 175

Ser Gly Ile Ser Pro Ile Pro Leu Phe Ser His Phe Thr Ala Asn Gln
            180                 185                 190

Ala Ile Leu Asp Ser Leu Ser Ser Gln Ser Ser Ser Pro Phe Val His
        195                 200                 205

Val Val Asp Phe Glu Ile Gly Phe Gly Gly Gln Tyr Ala Ser Leu Met
    210                 215                 220

Arg Glu Ile Ala Glu Lys Ser Ala Asn Gly Gly Phe Leu Arg Val Thr
225                 230                 235                 240

Ala Val Val Ala Glu Asp Cys Ala Val Glu Thr Arg Leu Val Lys Glu
            245                 250                 255

Asn Leu Thr Gln Phe Ala Ala Glu Met Lys Ile Arg Phe Gln Ile Glu
        260                 265                 270

Phe Val Leu Met Lys Thr Phe Glu Ile Leu Ser Phe Lys Ala Ile Arg
        275                 280                 285

Phe Val Asp Gly Glu Arg Thr Val Val Leu Ile Ser Pro Ala Ile Phe
    290                 295                 300

Arg Arg Val Ile Gly Ile Ala Glu Phe Val Asn Asn Leu Gly Arg Val
305                 310                 315                 320

Ser Pro Asn Val Val Val Phe Val Asp Ser Glu Gly Cys Thr Glu Thr
            325                 330                 335

Ala Gly Ser Gly Ser Phe Arg Arg Glu Phe Val Ser Ala Phe Glu Phe
        340                 345                 350

Tyr Thr Met Val Leu Glu Ser Leu Asp Ala Ala Ala Pro Pro Gly Asp
        355                 360                 365

Leu Val Lys Lys Ile Val Glu Thr Phe Leu Leu Arg Pro Lys Ile Ser
    370                 375                 380

Ala Ala Val Glu Thr Ala Ala Asn Arg Arg Ser Ala Gly Gln Met Thr
385                 390                 395                 400

Trp Arg Glu Met Leu Cys Ala Ala Gly Met Arg Pro Val Gln Leu Ser
                405                 410                 415

Gln Phe Ala Asp Phe Gln Ala Glu Cys Leu Leu Glu Lys Ala Gln Val
            420                 425                 430

Arg Gly Phe His Val Ala Lys Arg Gln Gly Glu Leu Val Leu Cys Trp
        435                 440                 445
```

29

```
His Gly Arg Ala Leu Val Ala Thr Ser Ala Trp Arg Phe
    450                 455             460
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<210> 82

<211> 486

<212> PRT

<213> aa seq of atSCL15

<400> 82

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Met Lys Ile Pro Ala Ser Ser Pro Gln Asp Thr Thr Asn Asn Asn Asn
1               5               10              15

Asn Thr Asn Ser Thr Asp Ser Asn His Leu Ser Met Asp Glu His Val
            20              25              30

Met Arg Ser Met Asp Trp Asp Ser Ile Met Lys Glu Leu Glu Leu Asp
        35              40              45

Asp Asp Ser Ala Pro Asn Ser Leu Lys Thr Gly Phe Thr Thr Thr Thr
    50              55              60

Thr Asp Ser Thr Ile Leu Pro Leu Tyr Ala Val Asp Ser Asn Leu Pro
65              70              75              80

Gly Phe Pro Asp Gln Ile Gln Pro Ser Asp Phe Glu Ser Ser Ser Asp
                85              90              95

Val Tyr Pro Gly Gln Asn Gln Thr Thr Gly Tyr Gly Phe Asn Ser Leu
            100             105             110

Asp Ser Val Asp Asn Gly Gly Phe Asp Phe Ile Glu Asp Leu Ile Arg
        115             120             125

Val Val Asp Cys Val Glu Ser Asp Glu Leu Gln Leu Ala Gln Val Val
    130             135             140

Leu Ser Arg Leu Asn Gln Arg Leu Arg Ser Pro Ala Gly Arg Pro Leu
145             150             155             160

Gln Arg Ala Ala Phe Tyr Phe Lys Glu Ala Leu Gly Ser Phe Leu Thr
            165             170             175

Gly Ser Asn Arg Asn Pro Ile Arg Leu Ser Ser Trp Ser Glu Ile Val
        180             185             190

Gln Arg Ile Arg Ala Ile Lys Glu Tyr Ser Gly Ile Ser Pro Ile Pro
        195             200             205

Leu Phe Ser His Phe Thr Ala Asn Gln Ala Ile Leu Asp Ser Leu Ser
    210             215             220

Ser Gln Ser Ser Ser Pro Phe Val His Val Val Asp Phe Glu Ile Gly
225             230             235             240

Phe Gly Gly Gln Tyr Ala Ser Leu Met Arg Glu Ile Thr Glu Lys Ser
            245             250             255
```

30

```
Val Ser Gly Gly Phe Leu Arg Val Thr Ala Val Val Ala Glu Glu Cys
            260                 265                 270

Ala Val Glu Thr Arg Leu Val Lys Glu Asn Leu Thr Gln Phe Ala Ala
            275                 280                 285

Glu Met Lys Ile Arg Phe Gln Ile Glu Phe Val Leu Met Lys Thr Phe
        290                 295                 300

Glu Met Leu Ser Phe Lys Ala Ile Arg Phe Val Glu Gly Glu Arg Thr
305                 310                 315                 320

Val Val Leu Ile Ser Pro Ala Ile Phe Arg Arg Leu Ser Gly Ile Thr
                325                 330                 335

Asp Phe Val Asn Asn Leu Arg Arg Val Ser Pro Lys Val Val Val Phe
            340                 345                 350

Val Asp Ser Glu Gly Trp Thr Glu Ile Ala Gly Ser Gly Ser Phe Arg
            355                 360                 365

Arg Glu Phe Val Ser Ala Leu Glu Phe Tyr Thr Met Val Leu Glu Ser
    370                 375                 380

Leu Asp Ala Ala Ala Pro Pro Gly Asp Leu Val Lys Lys Ile Val Glu
385                 390                 395                 400

Ala Phe Val Leu Arg Pro Lys Ile Ser Ala Ala Val Glu Thr Ala Ala
                405                 410                 415

Asp Arg Arg His Thr Gly Glu Met Thr Trp Arg Glu Ala Phe Cys Ala
            420                 425                 430

Ala Gly Met Arg Pro Ile Gln Gln Ser Gln Phe Ala Asp Phe Gln Ala
            435                 440                 445

Glu Cys Leu Leu Glu Lys Ala Gln Val Arg Gly Phe His Val Ala Lys
    450                 455                 460

Arg Gln Gly Glu Leu Val Leu Cys Trp His Gly Arg Ala Leu Val Ala
465                 470                 475                 480

Thr Ser Ala Trp Arg Phe
                485
```

<210> 83

<211> 536

<212> PRT

<213> aa seq lsSCR

<400> 83

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Met Lys Val Pro Phe Ser Thr Asn Asp Asn Val Ser Ser Lys Pro Leu
1               5                   10                  15

Val Asn Ser Asn Asn Ser Phe Thr Phe Pro Ala Ala Thr Asn Gly Ser
            20                  25                  30
```

```
Asn Leu Cys Tyr Glu Pro Lys Ser Val Leu Glu Leu Arg Arg Ser Pro
         35              40              45

Ser Pro Ile Val Asp Lys Gln Ile Ile Thr Thr Asn Pro Asp Leu Ser
     50              55              60

Ala Leu Cys Gly Gly Glu Asp Pro Leu Gln Leu Gly Asp His Val Leu
65              70              75              80

Ser Asn Phe Glu Asp Trp Asp Ser Leu Met Arg Glu Leu Gly Leu His
             85              90              95

Asp Asp Ser Ala Ser Leu Ser Lys Thr Asn Pro Leu Thr His Ser Glu
             100             105             110

Ser Leu Thr Gln Phe His Asn Leu Ser Glu Phe Ser Ala Glu Ser Asn
         115             120             125

Gln Phe Pro Ser Pro Asp Phe Ser Phe Ser Asp Thr Asn Phe Pro Gln
     130             135             140

Gln Phe Pro Thr Val Asn Gln Ala Ser Phe Ile Asn Ala Leu Asp Leu
145             150             155             160

Ser Gly Asp Ile His Gln Asn Trp Ser Val Gly Phe Asp Tyr Val Asp
             165             170             175

Glu Leu Ile Arg Phe Ala Glu Cys Phe Glu Thr Asn Ala Phe Gln Leu
         180             185             190

Ala His Val Ile Leu Ala Arg Leu Asn Gln Arg Leu Arg Ser Ala Ala
         195             200             205

Gly Lys Pro Leu Gln Arg Ala Ala Phe Tyr Phe Lys Glu Ala Leu Gln
     210             215             220

Ala Gln Leu Ala Gly Ser Ala Arg Gln Thr Arg Ser Ser Ser Ser Ser
225             230             235             240

Asp Val Ile Gln Thr Ile Lys Ser Tyr Lys Ile Leu Ser Asn Ile Ser
             245             250             255

Pro Ile Pro Met Phe Ser Ser Phe Thr Ala Asn Gln Ala Val Leu Glu
             260             265             270

Ala Val Asp Gly Ser Met Leu Val His Val Ile Asp Phe Asp Ile Gly
         275             280             285

Leu Gly Gly His Trp Ala Ser Phe Met Lys Glu Leu Ala Asp Lys Ala
     290             295             300

Glu Cys Arg Lys Ala Asn Ala Pro Ile Leu Arg Ile Thr Ala Leu Val
305             310             315             320

Pro Glu Glu Tyr Ala Val Glu Ser Arg Leu Ile Arg Glu Asn Leu Thr
             325             330             335

Gln Phe Ala Arg Glu Leu Asn Ile Gly Phe Glu Ile Asp Phe Val Leu
         340             345             350

Ile Arg Thr Phe Glu Leu Leu Ser Phe Lys Ala Ile Lys Phe Met Glu
         355             360             365
```

32

```
Gly Glu Lys Thr Ala Val Leu Leu Ser Pro Ala Ile Phe Arg Arg Val
    370                 375             380
```

```
Gly Ser Gly Phe Val Asn Glu Leu Arg Arg Ile Ser Pro Asn Val Val
385                 390             395                     400
```

```
Val His Val Asp Ser Glu Gly Leu Met Gly Tyr Gly Ala Met Ser Phe
            405             410                 415
```

```
Arg Gln Thr Val Ile Asp Gly Leu Glu Phe Tyr Ser Thr Leu Leu Glu
            420             425             430
```

```
Ser Leu Glu Ala Ala Asn Ile Gly Gly Gly Asn Cys Gly Asp Trp Met
    435                 440             445
```

```
Arg Lys Ile Glu Asn Phe Val Leu Phe Pro Lys Ile Val Asp Met Ile
    450                 455             460
```

```
Gly Ala Val Gly Arg Arg Gly Gly Gly Gly Ser Trp Arg Asp Ala Met
465                 470             475                     480
```

```
Val Asp Ala Gly Phe Arg Pro Val Gly Leu Ser Gln Phe Ala Asp Phe
            485             490                 495
```

```
Gln Ala Asp Cys Leu Leu Gly Arg Val Gln Val Arg Gly Phe His Val
            500             505             510
```

```
Ala Lys Arg Gln Ala Glu Met Leu Leu Cys Trp His Asp Arg Ala Leu
    515                 520             525
```

```
Val Ala Thr Ser Ala Trp Arg Cys
    530             535
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<210> 84

<211> 26

<212> DNA

<213> BnSCL1 sense primer

<400> 84
gatggacgaa catgccatgc gttcca   26

<210> 85

<211> 21

<212> DNA

<213> BnSCL1 anti-sense primer

<400> 85
cgctcggatc ttctgaacaa t   21

<210> 86

<211>   21

<212>   DNA

<213>   BnIAA1 sense primer

<400>   86
ccacgcgtcc ggtacgatga t   21

<210>   87

<211>   22

<212>   DNA

<213>   BnIAA1 anti-sense primer

<400>   87
gaagttgaga aatggtttat ga   22

<210>   88

<211>   21

<212>   DNA

<213>   BnIAA12 sense primer

<400>   88
acgctggtgc ttctcctcct c   21

<210>   89

<211>   24

<212>   DNA

<213>   BNIAA12 anti-sense primer

<400>   89
aaaacccatt agaagaacca agaa   24

<210>   90

<211>   33

<212>   DNA

<213>   forward primer for BnSCL1, BnSCL1 1-358, BnSCL1 1-261, BnSCL1 1-217
and BnSCL1 1-145 for pET-28b vector

<400>   90
gcaagcttat ggacgaacat gccatgcgtt cca   33

<210>   91

<211>   29

<212>   DNA

<213>   reverse primer for BnSCL1 for pET-28b vector

<400>   91
cgctcgagaa agcgccacgc tgacgtggc   29

<210>   92

<211>   29

<212>   DNA

<213>   reverse primer for BnSCL1 1-358 for pET-28b vector

<400>   92
cgctcgagcg cggagatctt cggacgtaa   29

<210>   93

<211>   29

<212>   DNA

<213>   reverse primer for BnSCL1 1-261 for pET-28b vector

<400>   93
cgctcgagcc taatcgcctt gaaagataa   29

<210>   94

<211>   29

<212>   DNA

<213>   reverse primer for BnSCL1 1-217 for pET-28b vector

<400>   94
cgctcgagcg ccacaaccgc cgtgactct   29

35

<210> 95

<211> 29

<212> DNA

<213> reverse primer for BnSCL1 1-145 for pET-28b vector

<400> 95
cgctcgagcg ctcggatctt ctgaacaat　　　　　　　　　　　　　　　29

<210> 96

<211> 34

<212> DNA

<213> forward primer for BnSCL1, BnSCL1 1-358, BnSCL1 1-261, BnSCL1 1-217
and BnSCL1 1-145 for PC86 vector

<400> 96
gcgtcgacga tggacgaaca tgccatgcgt tcca　　　　　　　　　　　34

<210> 97

<211> 30

<212> DNA

<213> forward primer for BnSCL1 146-358 for PC86 vector

<400> 97
gcgtcgacga ttaaggagtt ttccggtata　　　　　　　　　　　　　30

<210> 98

<211> 30

<212> DNA

<213> forward primer for BnSCL1 218-434 for PC86 vector

<400> 98
gcgtcgacgg aggattgcgc cgtcgagacg　　　　　　　　　　　　30

<210> 99

<211> 31

<212> DNA

<213>   reverse primer for BnSCL1 and BnSCL1 218-434 for PC86 vector

<400> 99
gcgcggccgc aaagcgccac gctgacgtgg c   31

<210> 100

<211> 31

<212> DNA

<213>   reverse primer for BnSCL1 1-358 for PC86 vector

<400> 100
gcgcggccgc cgcggagatc ttcggacgta a   31

<210> 101

<211> 31

<212> DNA

<213>   reverse primer for BnSCL1 1-261 for PC86 vector

<400> 101
gcgcggccgc cctaatcgcc ttgaaagata a   31

<210> 102

<211> 31

<212> DNA

<213>   reverse primer for BnSCL1 1-217 for PC86 vector

<400> 102
gcgcggccgc cgccacaacc gccgtgactc t   31

<210> 103

<211> 31

<212> DNA

<213>   reverse primer of BnSCL1 1-145 for PC86 vector

<400> 103
gcgcggccgc cgctcggatc ttctgaacaa t   31

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<210>   104

<211>   5

<212>   PRT

<213>   aa seq of LXXLL motif (148LGSLL152)


<400>   104

Leu Gly Ser Leu Leu
1               5
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